Original Research Article

Diversity analysis in Avocado (*Persea americana* Mill.) accessions of Lower Pulney Hills of Tamil Nadu, India.

Gopi.V[1*]., M.Ananthan[2]., M.S.Aneesa Rani[1]., M.Kumar[3]., P.Jeyakumar[4] and V.Krishnamoorthy[5]

[1* & 1]Department of Fruit Science, TNAU, Coimbatore, Tamil Nadu, India.

[2]Directorate of Open Distance and Learning, TNAU, Coimbatore, Tamil Nadu, India.

[3]Department of Genetics and Plant Breeding, TNAU, Coimbatore, Tamil Nadu, India.

[4]Department of Crop Physiology, TNAU, Coimbatore, Tamil Nadu, India.

[5] Department of Fruit Science HC&RI(W), TNAU, Trichy, Tamil Nadu, India.

Abstract

Avocado (*Persea americana* Mill.) is one of the world's most important subtropical fruit crops. So far, it's collection, systematic evaluation and utilization studies are limited and this would be perhaps the first systematic study to quantify the variability available. This investigation of genetic diversity would be a first in Tamil Nadu. Morphological diversity in qualitative and quantitative traits of avocado genotypes investigated in this study using the International Plant Genetic Resources Institute descriptors to evaluate twenty accessions. The traits evaluated were related to leaf, flowering, fruit, seed, and yield traits. The 20 genotypes were classified into ten groups using Mahalanobis statistics. PA-56 and PA-68, which differ in terms of characteristics and distance, might provide transgressive segregants upon curing to resistance desirable traits. Principal component analysis was done to assess the qualitative and quantitative characters combination. The total variability defined by the five PCs was 84.14 percent, whereas the variability of the 13 primary components was 99.99 percent. The genotypes that could be chosen based on PC values in each constituent graph that were positive and > 1.0 in each PC and a combination away that would unravel many genetic patterns. Findings of this research will aid in germplasm management, conservation, and breeding strategies.

Keywords : Avocado, Diversity, genotypes, principal component and descriptors.

Introduction

Butter fruit, popularly known as *Persea americana*, is a flowering plant of the Lauraceae family. (Drecher, 2013). It has a diploid chromosomal number of 2n = 24 and is considered to have originated in Mexico and Central America (Rohwer, 1999). Its nutrient composition is comparable to ripe olives, which contains 2.1 percent protein and 24-26 percent fat on average. Since the fruit has less than 1% sugar, diabetic people may also prefer to eat it as a high-energy diet. It's also used in cosmetics. Botanically, the fruit is a large berry with a single seed. The avocado was imported to India from Sri Lanka in the nineteenth century (Ghosh *et al*., 2000). The cultivated crop is now available in three botanical varieties or subspecies. Described as Mexican (*P. Americana* var. *drymifolia*), Guatemalan (*P. americana* var. G*uatemalensis* Wms.) and West Indian (*P. americana* var. *americana* Mill.) (Bergh and Scora, 1973).

Avocados are extensively produced in the Western Ghats of Tamil Nadu's Lower Pulney hills, where they are grown at an elevation of 800-1600 metres above sea level. Avocado plants are heterozygous in nature owing to cross pollination. Unfortunately, due to a lack of research in this crop, knowledge on its genetic diversity is currently limited. In this stage, avocado's diversity was assessed by using International Plant Genetic Resources Institute descriptors for qualitative and quantitative traits (Tree, leaf, flowering, fruit and seed characteristics). However, research is being conducted to assess the diversity of seed-propagated avocado cultivated in Lower Pulney Hills. The findings of this study will aid in the design of germplasm management and conservation, as well as breeding strategies.

Materials and Methods

The exploration was conducted in six locations in Tamil Nadu's Lower Pulney hills. The genotypes were collected from Uthu, Patlakadu, Thandigudi, Peruganal, Thadiyankudisai, Manjalparappu and Tamil Nadu Agricultural University, orchard, Coimbatore, which forms the Western Ghats which are located between 800 and 1600 metres above sea level (Msl) at 10 degrees south latitude and 77 degrees east longitude. These areas were chosen because of the exists trees number of avocado trees. Old avocado trees grown from seeds are referred to as seedling progenies. Field visits were undertaken with the assistance of locals who were familiar with avocado production sites in a specific area during August 2019 to October 2020. For the identified trees information on the farmer's name, name of the village, district, and location where gathers and the tree was identified. The site's latitude, longitude, and elevation (altitude) were calculated using a Garmin Epic GPS (Global positioning system) mapping & Multisport Watch.

Table 1 contains information about the collected accessions. Trees were designated as accessions PA - 51 to PA – 70 and observed for leaf, flower, fruit, seed, and yield characteristics using the descriptors developed by the International Plant Genetic Resources Institute (IPGRI; now Bio-diversity International),Rome, Italy in 2000.

The observations were made on fruit five randomly selected fruits from each accession when they were fully mature. The avocado descriptor was used to describe the tree shape, tree age, tree height (m), tree canopy (m^2), trunk circumference (cm), leaf blade length (cm), number of flower / inflorescence, fruit length (cm), fruit circumference (cm), fruit weight (g), fruit peel thickness (mm), pulp peel ratio, seed weight (g), seed - pulp ratio, length of seed cavity (cm), length of seed (cm), seed circumference (cm).

The clustering groups were constructed based on the neighbour joining approach using a dissimilarity matrix of the 20 avocado genotypes using the R programme – 4.1.2 version. Principal components (PCs) with an eigenvalue greater than one were chosen

(Jeffers, 1967) and the Principal Component Analysis was carried out using standardised values from the PAST 3 application. The scree plot was used to visually examine the components that contributed most to the total variation.

Results and Discussion

Cluster analysis

A cluster analysis classifies a natural population of the same species into closely related phylogenetic main groups and subgroups. This approach groups the population using a set of morphological traits with very consistent criteria. In this study, the properties of the tree, leaves, flowers, fruits, and seeds were used to evaluate their characters. Based on 38 morphological traits, a dendrogram displays the relationships between all avocado trees.

The twenty genotypes were classified into ten groups (Table 2 and Fig 1). Cluster VII had the most genotypes (6), followed by cluster V (3), cluster II (2), cluster IV (2), cluster VI (2), cluster I,III,VIII, IX, had each one. Cluster seven had..... genotypes which could be due to the same set of planting materials being exchanged the study region. and that there should be less morphological diversity in these places. Avocado accessions with comparable morphological characteristics were classified together, so samples viz., PA-70, PA-62, PA-63, PA-61, PA-69, and PA-51 were grouped together, followed by groups II, IV, V, VI. All the groups are separated at 12% similarity coefficient level. In future, while crossing the genotypes *viz.*, PA-56 and PA-68 which possess variations in the characters and distance between the two genotypes are diverse in nature can give new combination of characters. The genotypes PA-56 and PA-68 showed higher variation since these were propagated through seeds.

Principal component analysis (PCA)

PCA is an effective approach for identifying the fewest number of components, which aids in predicting maximum variability out of total variability (Morrison, 1992). The PCA provides additional feature of ranking genotypes based on PC scores. PCA was used to analyse 20 qualitative and 17 quantitative characters. The data showed that there are five principal components with eigenvalues greater than one (Table.3). However, there are also thirteen principal components expressed (Table.4). The variability reported in the five PCs was 84.14 percent (Table.3).The variability reported in the 13 principal components was 99.99 percent (Table. 4). Chaimae Nasri *et al*., (2021) discovered that two principal components with multiple eigenvalues accounted for the majority of the variance in avocado oil.

In a Scree plot graph, the component number was plotted on the X-axis, and the eigenvalues were plotted on the Y-axis (Fig.2a). It explained the percentage of variance associated with qualitative features for each primary component. Gour *et al.,* (2017) discovered that PC1 had a maximum variability of 28.0 percent with an eigenvalue of 6.79, which subsequently decreased. The quantitative characteristics were expressed as having more variability in PC1 92.45 percent with eigenvalues of 44201.4. (Fig 2b). These findings can be used to create appropriate selection indices by explaining each PC and understanding it's intensity. PCA study on 20 avocado genotypes resulted in the measurement of qualitative and quantitative features based on principal component scores (PC scores). The genotype with the highest PC score in that PC indicates the maximum values for the variables in that genotype. PC1 components included six genotypes *viz*., PA - 55, PA - 56, PA - 58, PA - 59, PA - 65, PA - 66). PC2 components included genotypes with > 1.0 values (PA-60, PA - 61, PA - 64, PA - 65, PA - 66, PA - 70), and PC3 component had five genotypes *viz.*, PA -52, PA - 54, PA - 58, PA - 65, PA - 68).The maximum values for the variables in a particular genotype are indicated by the genotype with the highest PC score in that PC (Table 8). PC1 components was had (PA -52,PA- 53, PA - 56, PA -66, PA -67), PC2 components consist of

(PA -51, PA -52, PA -54, PA - 55, PA -56, PA-57, PA - 58, PA -59, PA -60, PA -61), PC3 components include genotypes (PA-56, PA -57, PA - 58, PA - 59, PA -60, PA -61, PA - 62, PA - 67, PA -69.

Figure 3 showed a scatter plot including PC1 and PC2 which revealed a distinct pattern of clustering among the 20 avocado genotypes. PA - 60, PA - 65, PA - 55, PA - 53, PA - 67, PA - 62, PA -70 are the genotypes that inhabited the convex of the hull. The maximum variation was observed in bitterness of pulp, tree shape, gloss of fruit skin, fruit shape. Principal components, scatter plot had PC1 and PC3, maximum variability was noticed among the accessions namely PA - 65, PA - 58, PA - 55, PA - 66, PA - 64,PA - 67, PA - 62,PA -70, PA -52 for the characters viz., bitterness of pulp, tree shape and length of seed .

Scatter plot incorporating PC1 and PC2indicated a clear pattern of clustering among the 20 avocado genotypes. The genotypes which occupied the convex of the hull are PA - 52, PA -56, PA - 67, PA - 62, PA - 63, PA - 66, PA - 69, PA -58. By the results of principal components, scatter plot for PC1 and PC2, the maximum variation was observed for tree height, trunk circumference, yield, number of flower / inflorescence (Fig. 4). Paz-Vega *et al*. 1997 discovered the tropical avocado fruit weight 200 to 300 g fresh weight, in the study fruit sampled weighed between 220and 370g. Majority of the fruits had ski thickness with a few thick skin thickness is a characteristic feature of west Indian species.

Principal components , scatter plot for PC1 and PC3, maximum diversity was noticed in the accessions PA -67, PA - 56, PA -60, PA -63, PA -54, PA - 58,PA - 59 for the characters *viz.*, tree height, trunk circumference, number of flower / inflorescence and yield.

Based on the findings of this study, it is concluded that a broad range of variability exists among the genotypes for all of the feature studied in the accessions especially of PA - 56 and PA-68. These accessions can be exploited for improving avocado genotypes by clonal selection. After they can also be employed in crossings for recovering recombination's.

According to the principal component analysis, the traits such as of tree shape, fruit shape, leaf shape, tree age, tree height, leaf blade length, number of flower/inflorescence, fruit length, fruit circumference, fruit weight, fruit peel thickness, pulp – peel ratio, yield should be given preference for selection of superior genotypes.

Reference :

Bergh, B.O., Scora, R.W. and Storey, W.B. (1973) A comparison of leaf terpenes in *Persea* subgenus *Persea.Botanical Gazette* 134, 130–134.

Chaimae Nasr, YasminaHalabi, HichamHarhar, Faez Mohammed., AbdelkabirBellaouchou, AbdallahGuenbour and Mohamed Tabyaoui. (2021). Chemical characterization of oil from four avocado varieties cultivated in Morocco, Ocl 28:19.

Drecher, M.L. Davenport AJ. (2013). Hass avocado composition andpotential health effects. Crit. Rev. Food Sci. Nutr. 53:738-750.

Ghosh, S.P, *et al*., (2000). Avocado Production in Asia and the Pacific. FAO Corporate Document Repository.

Gour, L. Maurya, S.B, Koutu, G.K., Singh, S.K, Shukla, S.S. and Mishra, D.K. 2017. Characterization of Rice (*Oryzasativa* L.) genotypes using principal component analysis including scree plot & rotated component matrix. *International journal of chemical studies*, 5(4): 975- 83.

International Plant Genetic Resources Institute (IPGRI).1995. Descriptors for Avocado (Persea spp.); International Plant Genetic Resources Institute: Rome, Italy, pp. 1-52.

Jeffers, J.N. 1967. Two case studies in the application of principal component analysis. *Journal of the Royal Statistical Society* : Series C (*Applied Statistics*), 16(3):225-236.

Morrison, D.E. 1982. Multivariate statistical methods (2nd ed. 4 th print,1978). Mcgraw Hill kogakusta Ltd

Rohwer, JG, Kubitzki, K, Rohwer, J, Bittrich V.1993. The families and genera of flowering plants. Springer, Berlin. 75(3):426-437.

Paz-vega, S.1997. Alternate bearing in the avocado (*Persea americana* Mill.).California Avocado Society Yearbook 81:117-148.

Table -1: Details of exploration Avocado (*Persea americana* Mill.) genotypes from Lower pulney hills of Tamil Nadu and Coimbatore.

Accession Number	Name of the genotypes	Source / Location	Tree age (years)	Latitude	Longitude
PA-51	Uthu local	S. Ravi, Uthu	20	10.367	77.980
PA-52	Uthu local	S. Ravi, Uthu	12	10.367	77.980
PA-53	Uthu local	S. Ravi, Uthu	13	10.367	77.980
PA-54	Uthu local	S. Ravi, Uthu	15	10.367	77.980
PA-55	Patlakadu Local	R.Kariyammal, Patlakadu	18	10.225	77.667
PA-56	Thandigudi local	S.Moorthy, Thandigudi	22	10.306	77.645
PA-57	Thandigudi local	S.Moorthy, Thandigudi	14	10.306	77.645
PA-58	Peruganal local	S.Murali, Peruganal	14	10.300	77.671
PA-59	Peruganal local	S.Murali, Peruganal	24	10.300	77.671
PA-60	Peruganal local	S.Murali, Peruganal	24	10.300	77.671
PA-61	Thadiyankudisai local	Horticultural Research Station, Thadiyankudisai	16	10.296	77.708
PA-62	Thadiyankudisai local	Horticultural Research Station, Thadiyankudisai	8	10.296	77.708
PA-63	Thadiyankudisai local	Horticultural Research Station, Thadiyankudisai	8	10.296	77.708
PA-64	Manjalparppu local	S.Pradeep, Manjalparappu	8	10.301	77.751
PA-65	Manjalparappu local	S.Pradeep, Manjalparappu	28	10.301	77.751
PA-66	TNAU, Orchard, local	TNAU, Orchard,Coimbatore	30	11.011	76.935
PA-67	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	15	11.011	76.935
PA-68	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	12	11.011	76.935
PA-69	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	12	11.011	76.935
PA-70	TNAU, Orchard, local	TNAU, Orchard, Coimbatore	15	11.011	76.935

Table 2. Clustering of 20 Avocado genotypes

Cluster	Number of Genotypes	Name of the Genotypes
Cluster I	1	PA - 56
Cluster II	2	PA - 55, PA - 58
Cluster III	1	PA - 64
Cluster IV	2	PA - 54, PA - 60
Cluster V	3	PA - 52, PA- 53, PA - 57
Cluster VI	2	PA - 66, PA - 67
Cluster VII	6	PA - 51, PA - 69, PA - 61, PA - 63, PA - 62, PA -70
Cluster VIII	1	PA - 65
Cluster IX	1	PA - 59
Cluster X	1	PA - 68

Table 3.Eigenvalues, variance, cumulative variability and qualitative characters of avocado genotypes

Principal component	Eigenvalue	Per cent variance	Cumulative variance
1	6.79163	28.068	28.068
2	5.26583	21.762	49.83
3	4.02047	16.615	66.445
4	2.68017	11.076	77.521
5	1.60178	6.6196	84.1406

Table 4.Eigenvalues, variance, cumulative variability and quantitative characters of avocado genotypes

Principal component	Eigenvalue	Per cent variance	Cumulative variance
1	44201.4	92.454	92.454
2	1656.96	3.465	95.919
3	999.43	2.090	98.010
4	553.01	1.156	99.167
5	305.74	0.639	99.806
6	34.61	0.072	99.878
7	20.86	0.043	99.922
8	15.097	0.031	99.954
9	9.802	0.020	99.974
10	4.279	0.008	99.983
11	3.795	0.007	99.991
12	2.004	0.004	99.995
13	1.727	0.003	99.999

Table 5. Interpretation of PCA for the qualitative traits having values > 0.5 in each PCs.

	PC 1	PC 2	PC 3
Traits	Tree shape Leaf shape Bitterness of pulp	Fruit shape	Bitterness of pulp

Table 6. Interpretation of PCA for the quantitative traits having values > 0.5 in each PCs.

	PC 1	PC 2	PC 3
Traits	Tree age Tree height Leaf blade length Number of flower/inflorescence Fruit length Fruit circumferencre Fruit weight Fruit peel thickness Pulp – Peel ratio Seed weight Length of seed cavity Length of seed Seed circumference Yield	Tree age Tree height Tree canopy Trunk circumference Pulp – Peel ratio Seed weight yield	Tree age Tree height Tree canopy Trunk circumference Number of flower/inflorescence

Table 7: Genotype selection based on PC score in each component with positive values and greater than 1.0 in each PC – Qualitative characters

PC1	PC2	PC3
PA-55 (4.9904)	PA -60 (5.2737)	PA - 52 (3.6393)
PA-56 (1.6045)	PA - 61 (1.6374)	PA - 54 (2.3931)
PA-58 (2.7251)	PA -64 (2.0327)	PA - 58 (2.5134)
PA- 59 (5.7829)	PA - 65 (4.0907)	PA - 65 (3.0955)
PA -65 (1.3762)	PA -66 (1.6068)	PA - 68 (3.0498)
PA -66 (2.1367)	PA - 70 (1.2148)	

Table 8.Genotype selection based on PC score in each component with positive values and greater than 1.0 in each PC – Quantitative characters

PC1	PC2	PC3
PA-52 (29.325)	PA -51 (35.181)	PA -56 (1.7008)
PA - 53 (276.89)	PA - 52 (67.609)	PA - 57 (19.388)
PA-56 (772.11)	PA -54 (15.34)	PA - 58 (32.725)
PA -66 (24.012)	PA - 55 (8.5106)	PA - 59 (45.678)
PA -67 (123.9)	PA -56 (26.395)	PA - 60 (39.847)
	PA - 57 (28.472)	PA - 61 (43.407)
	PA - 58 (37.359)	PA - 62 (17.292)
	PA - 59 (41.601)	PA - 67 (55.631)
	PA - 60 (47.04)	PA - 69 (4.0045)
	PA - 61 (20.1)	

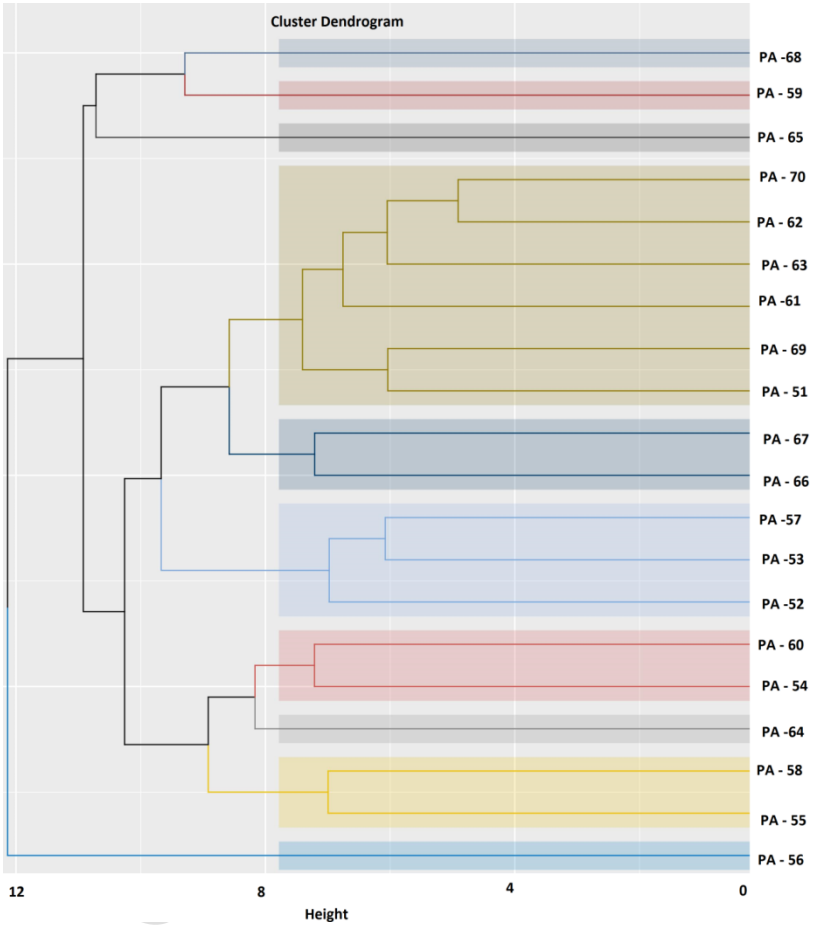

Fig 1. Dendrogram based on the neighbour joining algorithm using a dissimilarity matrix of the 20 avocado genotypes

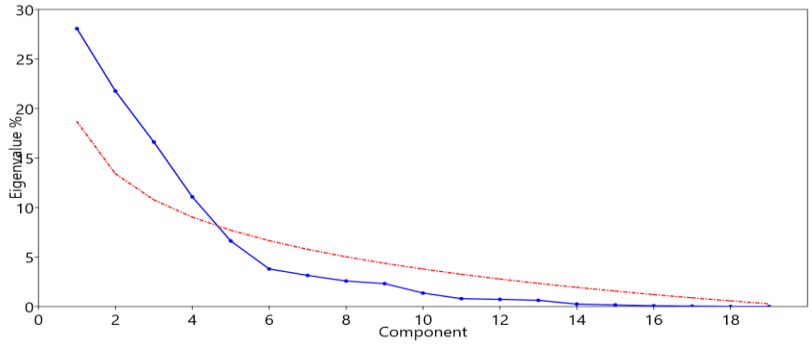

Fig 2a . Scree plot based on eigen values of qualitative characters

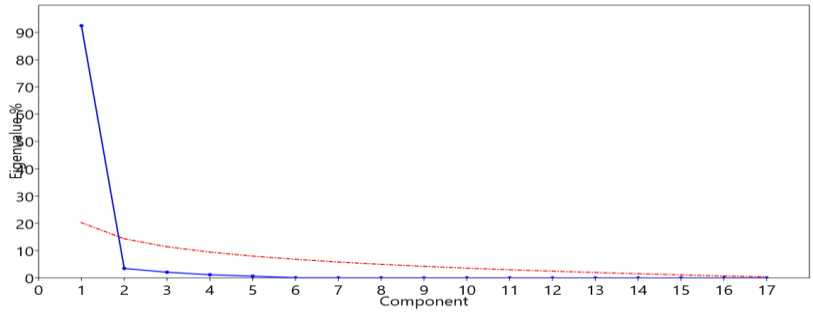

Fig 2b . Scree plot based on eigen values of quantitative characters

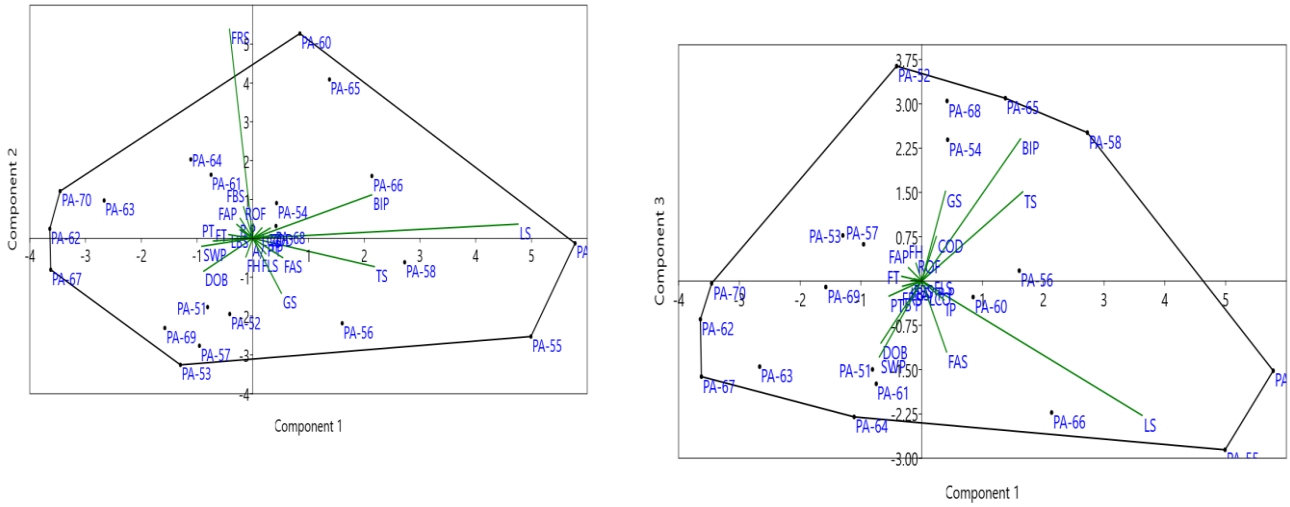

Fig 3. Genotype scatterplot illustrating the relationship between qualitative traits of PC1 and PC2, PC1 and PC3

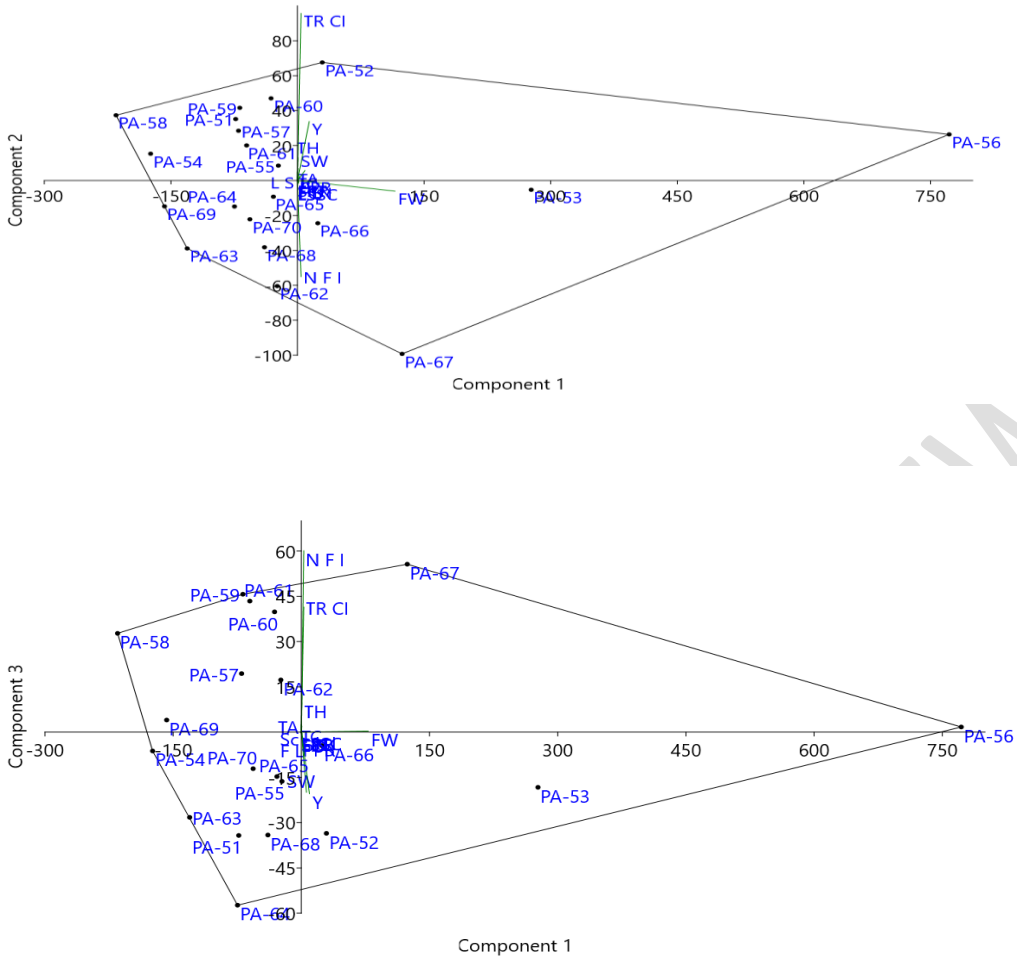

Fig 3. Genotype scatterplot illustrating the relationship between quantitative traits ofPC1 and PC2, PC1 and PC3